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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/308,830A

DATE: 04/16/2002

TIME: 11:31:36

Input Set : A:\600-346SeqLst.txt

Output Set: N:\CRF3\04162002\I308830A.raw

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3 <110> APPLICANT: Schlievert, Patrick M.
4      Roggiani, Manuela
5      Auge, Jennifer Stoehr
6      Ohlendorf, Douglas
8 <120> TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
10 <130> FILE REFERENCE: 600.346USWO
12 <140> CURRENT APPLICATION NUMBER: US 09/308,830A
13 <141> CURRENT FILING DATE: 1999-08-04
15 <150> PRIOR APPLICATION NUMBER: PCT/US97/22228
16 <151> PRIOR FILING DATE: 1997-12-05
18 <150> PRIOR APPLICATION NUMBER: US 60/032,930
19 <151> PRIOR FILING DATE: 1996-12-06
21 <160> NUMBER OF SEQ ID NOS: 13
23 <170> SOFTWARE: PatentIn version 3.1
25 <210> SEQ ID NO: 1
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28 <213> ORGANISM: Streptococcus sp.
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53 atttccataa atattaataa ataattaaaa ataaaataat aaataattaa tc          172
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69 <210> SEQ ID NO: 5

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77 taaatatata aataaaataa ttacatatta aaaataatac ttaattataa aaacactata	120
79 atttccataa atattaataa ataattaaaa ataaaataat aaataattaa tc	172
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84 <212> TYPE: DNA	
85 <213> ORGANISM: Streptococcus sp.	
87 <400> SEQUENCE: 6	
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90 taaatatata aataaaataa ttacatatta aaaataatac ttaattataa aaacactata	120
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148 <211> LENGTH: 31	

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163 <222> LOCATION: (828)..(1580)
164 <223> OTHER INFORMATION:
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170 ttatcccttg aaacaggtgc aacatagatt agggcatgga gatttaccag acaactatga 120
172 acgtatatac tcacatcacy caatcgccaa ttgatgacat tggactaaa ttcaatcaat 180
174 ttgttactaa caagcaacta gattgacaac taattctcaa caaacgttaa tttaacaaca 240
176 ttcaagtaac tcccaccagc tccatcaatg cttaccgtaa gtaatcataa cttactaaaa 300
178 ccttggtaaca tcaaggtttt ttcttttgtt cttgttcatg agttaccata actttctata 360
180 ttattgacaa ctaaattgac aactcttcaa ttatTTTCT gtctactcaa agtttcttc 420
182 atttgatata gtctaattcc accatcactt cttccactct ctctaccgtc acaacttcat 480
184 catctctcac ttttcgtgt gtaacacat aatcaaataat ctttccgttt ttacgcacta 540
186 tcgctactgt gtcacccataa atataccct tatcaatcgc ttctttaaac tcacatataat 600
188 ataacatatt tcatcctcct acctatctat tcgtaaaaag ataaaaataa ctattgttt 660
190 ttttggtaattt ttataataaa attattaata taagttatg ttttttaaaa atatacaatt 720
192 ttattctatt tatagtttagc tatttttca ttgttagtaa tattggtaaa ttgtataaac 780
194 ctttttaaat ctagaggaga acccagatataaaatggagg aatatta atg gaa aac 836
195 Met Glu Asn
196 1
198 aat aaa aaa gta ttg aag aaa atg gta ttt ttt gtt tta gtg aca ttt 884
199 Asn Lys Lys Val Leu Lys Lys Met Val Phe Phe Val Leu Val Thr Phe
200 5 10 15
202 ctt gga cta aca atc tcg caa gag gta ttt gct caa caa gac ccc gat 932
203 Leu Gly Leu Thr Ile Ser Gln Glu Val Phe Ala Gln Gln Asp Pro Asp
204 20 25 30 35
206 cca agc caa ctt cac aga tct agt tta gtt aaa aac ctt caa aat ata 980
207 Pro Ser Gln Leu His Arg Ser Ser Leu Val Lys Asn Leu Gln Asn Ile
208 40 45 50
210 tat ttt ctt tat gag ggt gac cct gtt act cac gag aat gtg aaa tct 1028
211 Tyr Phe Leu Tyr Glu Gly Asp Pro Val Thr His Glu Asn Val Lys Ser
212 55 60 65
214 gtt gat caa ctt tta tct cac cat tta ata tat aat gtt tca ggg cca 1076
215 Val Asp Gln Leu Leu Ser His His Leu Ile Tyr Asn Val Ser Gly Pro
216 70 75 80
218 aat tat gat aaa tta aaa act gaa ctt aag aac caa gag atg gca act 1124
219 Asn Tyr Asp Lys Leu Lys Thr Glu Leu Lys Asn Gln Glu Met Ala Thr
220 85 90 95
222 tta ttt aag gat aaa aac gtt gat att tat ggt gta gaa tat tac cat 1172
223 Leu Phe Lys Asp Lys Asn Val Asp Ile Tyr Gly Val Glu Tyr Tyr His

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224	100	105	110	115	
226	ctc tgt tat tta tgt	gaa aat gca gaa agg agt gca tgt atc tac gga		1220	
227	Leu Cys Tyr Leu Cys	Glu Asn Ala Glu Arg Ser Ala Cys Ile Tyr Gly			
228	120	125	130		
230	ggg gta aca aat cat gaa ggg aat cat tta gaa att cct aaa aag ata			1268	
231	Gly Val Thr Asn His Glu Gly Asn His Leu Glu Ile Pro Lys Lys Ile				
232	135	140	145		
234	gtc gtt aaa gta tca atc gat ggt atc caa agc cta tca ttt gat att			1316	
235	Val Val Lys Val Ser Ile Asp Gly Ile Gln Ser Leu Ser Phe Asp Ile				
236	150	155	160		
238	gaa aca aat aaa aaa atg gta act gct caa gaa tta gac tat aaa gtt			1364	
239	Glu Thr Asn Lys Lys Met Val Thr Ala Gln Glu Leu Asp Tyr Lys Val				
240	165	170	175		
242	aga aaa tat ctt aca gat aat aag caa cta tat act aat gga cct tct			1412	
243	Arg Lys Tyr Leu Thr Asp Asn Lys Gln Leu Tyr Thr Asn Gly Pro Ser				
244	180	185	190	195	
246	aaa tat gaa act gga tat ata aag ttc ata cct aag aat aaa gaa agt			1460	
247	Lys Tyr Glu Thr Gly Tyr Ile Lys Phe Ile Pro Lys Asn Lys Glu Ser				
248	200	205	210		
250	ttt tgg ttt gat ttt ttc cct gaa cca gaa ttt act caa tct aaa tat			1508	
251	Phe Trp Phe Asp Phe Phe Pro Glu Pro Glu Phe Thr Gln Ser Lys Tyr				
252	215	220	225		
254	ctt atg ata tat aaa gat aat gaa acg ctt gac tca aac aca agc caa			1556	
255	Leu Met Ile Tyr Lys Asp Asn Glu Thr Leu Asp Ser Asn Thr Ser Gln				
256	230	235	240		
258	att gaa gtc tac cta aca acc aag taacttttg cttttgccaa ccttacctac			1610	
259	Ile Glu Val Tyr Leu Thr Thr Lys				
260	245	250			
262	tgctggattt agaaatttta ttgcaattct tttattaatg taaaaaccgc tcatttgatg			1670	
264	agcggttttgc tcttatctaa aggagctta cctcctaatttgc caaaaattttaatgtttg			1730	
266	gattttgtat tttgtctattt gtatttgatg ggtaatccccat ttttcgaca gacatcgatcg			1790	
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284	Val Thr Phe Leu Gly Leu Thr Ile Ser Gln Glu Val Phe Ala Gln Gln				
285	20	25	30		
288	Asp Pro Asp Pro Ser Gln Leu His Arg Ser Ser Leu Val Lys Asn Leu				
289	35	40	45		
292	Gln Asn Ile Tyr Phe Leu Tyr Glu Gly Asp Pro Val Thr His Glu Asn				
293	50	55	60		
296	Val Lys Ser Val Asp Gln Leu Leu Ser His His Leu Ile Tyr Asn Val				
297	65	70	75	80	
300	Ser Gly Pro Asn Tyr Asp Lys Leu Lys Thr Glu Leu Lys Asn Gln Glu				

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304 Met Ala Thr Leu Phe Lys Asp Lys Asn Val Asp Ile Tyr Gly Val Glu
305 100 105 110
308 Tyr Tyr His Leu Cys Tyr Leu Cys Glu Asn Ala Glu Arg Ser Ala Cys
309 115 120 125
312 Ile Tyr Gly Gly Val Thr Asn His Glu Gly Asn His Leu Glu Ile Pro
313 130 135 140
316 Lys Lys Ile Val Val Lys Val Ser Ile Asp Gly Ile Gln Ser Leu Ser
317 145 150 155 160
320 Phe Asp Ile Glu Thr Asn Lys Lys Met Val Thr Ala Gln Glu Leu Asp
321 165 170 175
324 Tyr Lys Val Arg Lys Tyr Leu Thr Asp Asn Lys Gln Leu Tyr Thr Asn
325 180 185 190
328 Gly Pro Ser Lys Tyr Glu Thr Gly Tyr Ile Lys Phe Ile Pro Lys Asn
329 195 200 205
332 Lys Glu Ser Phe Trp Phe Asp Phe Pro Glu Pro Glu Phe Thr Gln
333 210 215 220
336 Ser Lys Tyr Leu Met Ile Tyr Lys Asp Asn Glu Thr Leu Asp Ser Asn
337 225 230 235 240
340 Thr Ser Gln Ile Glu Val Tyr Leu Thr Thr Lys
341 245 250

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